ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

Figure 1A

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCATACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGGGAGCGGAAACAGGGAGAGCAGT

CTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACC

TTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGTGACCATGGTAGTTGGA

GCCTCAGTCCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGACCACCGACTCCGGCTCT

TCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAGTGCTGCCTCAAGGTGC

CAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTGGTTGTGTCTGACCGCA

GGCTGTACCTGTTGA

Figure 1B.

ATGTTCGGCTCCGCCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG

TTGTGGAAGCTCGCGGGGTTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC

ACCCTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG

GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC

CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACTCAAG

CTGGTCCATGTTGCTGGTCCTGGCCCCACAGGGCCCATCAAGATTTTCCCCTTCAAATCC

CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC

TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC

TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC

TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT

TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT

GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC

TCAGGGGCTGCTCTGGGGGTCCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC

CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTTGGCATACAACCTGCTGGAAGGACAC

CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC

CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCCAGTACTTGTCACCCCGGGCC

AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCACTGACAGATTTTCAG

ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCCACCTTTGCCCTGGCCAGTGGGGAGT

ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTTGTG

ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT

GAACCCAGTGATACGGACCCGGAGCCCCGAACTCTGAACCCCTCTCCGGCTGGATGGTTC

GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

Figure 2A

TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCCTCTGCCGGCCACCCCCACT

ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT

TCACCCCCGCAGGAGGAAGCCAGAGGCCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG

GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG

GGGGAGATGGTGGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC

CAGAAGGAAGTGGAAGCGGAACTCTGTCGCCCCTTGTTGGTGTGTCCCCTGGAGGGGCCT

GAGGGCGTACGGGGCAGGGAATGCTTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG

GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG

ATAGAGCCGGAGGCCCAGGCCCAGAGGTCGCCCAGGCCCACGGGCTCAGATCTGCTCCCT

GGAGCCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC

TATTTGGTGCTGGAGCCTGATGCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC

CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA

TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC

AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGTGTGTCCTAAC

TGTGGTAGTGACCACGTGGTTCTCCTCGCTGTGTCTCGGGGAACCCCCAACAGGGAGCGG

AAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCT

GGCCATGGTGACCACCTTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGT

GACCATGGTAGTTGGAGCCTCAGTCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGAC

CACCGACTCCGGCTCTTCCTGGATGTTGAGGTGTTCAGCGATGCCCAGGAGGAGTTCCAG

TGCTGCCTCAAGGTGCCAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTG

GTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGATGCGTGAGCCTCCA

GCTAGCTGGCTGCAGCTGACCCTGGCTGTTCCCCTGCAGGATCTGAGTGGCATAGAGCTG

Figure 2B

GGCCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGCAGCTGGGGCGGGCCGCTGTGTGCTG

CTGCCCCGAGATGCCAGGCATTGCCGGGCCTTCCTAGAGGAGCTCCTTGATGTCTTGCAG

TCTCTGCCCCCTGCCTGGAGGAACTGTGTCAGTGCCACAGAGGAGGAGGTCACCCCCCAG

CACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCCTTGGAGGCTCGCCAGTTCTTCTAC

CTTCGGGCGTTCCTGGTTGAAGGCCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCG

TCCACCCTGTTCCTGTTAGATGAGGATGCTGCAGGGTCCCCGGCAGAGCCCTCTCCTCCA

GCAGCATCTGGCGAAGCCTCTGAGAAGGTGCCTCCCTCGGGGCCGGGCCCTGCTGTGCGT

GTCAGGGAGCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCCT

GAGGACTTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTC

CGTGTGGTGTGTCAGGAGCAGCTGACAGCCCTGCTTGCCTGGATCCGGGAACCATGGGAG

GAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA

Figure 2C.

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

QKEVEAELCRPLLVCPLEGPEGIRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTGSGNRESS

LWLLLRLPALSATLLAMVTTLTGPRTAHLRHRAPVTMVVGASVPPLSAVASALWTTDSGS

SWMLRCSAMPRRSSSAASRCQWHWQATLGSSCALWLCLTAGCTC

Figure 3.

MFGSAPQRPVAMTTAQRDSLLWKLAGLLRESGDVVLSGCSTLSLLTPTLQQLNHVFELHL

GPWGPGQTGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGPTGPIKIFPFKS

LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN

FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGP

SGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN

PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSLTDFQTHTSLGLSPMGPPLPWPVGS

TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTDPEPRTLNPSPAGWF

VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP

SPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEAGEEEEEEQD

QKEVEAELCRPLLVCPLEGPEGVRGRECFLRVTSAHLFEVELQAARTLERLELQSLEAAE

IEPEAQAQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDAHAAVQELLAVLT

PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTESPAVCPN

CGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRAKNSPPQAPSTR

DHGSWSLSPPPERCGLRSVDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLV

VVSDRRLYLLKVTGEMREPPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGAGRCVL

LPRDARHCRAFLEELLDVLQSLPPAWRNCVSATEEEVTPQHRLWPLLEKDSSLEARQFFY

LRAFLVEGPSTCLVSLLLTPSTLFLLDEDAAGSPAEPSPPAASGEASEKVPPSGPGPAVR

VREQQPLSSLSSVLLYRSAPEDLRLLFYDEVSRLESFWALRVVCQEQLTALLAWIREPWE

ELFSIGLRTVIQEALALDR

Figure 4.

```
>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
           (AF082516) I-1 receptor candidate protein [Homo sapiens]
           Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
           +L  T  LK + V+G  GP G         P  +  FKSL  +E+       + GL
Sbjct: 180 ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
             L TL    S  +++E+L               +   G   + +P W AL + + S+N
Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

Query: 202 XXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                           HN +      L  L  L HLD+SYN+L  +  +       +
Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262 VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
            L L GN L SL GL +L +L +LDL  N +E   E+  +  L  L  + L  NPL   P
Sbjct: 359 TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322 EHRAATAQYLSPRARD 337
           ++R         RA +
Sbjct: 419 DYRTKVLAQFGERASE 434
```

Figure 5.

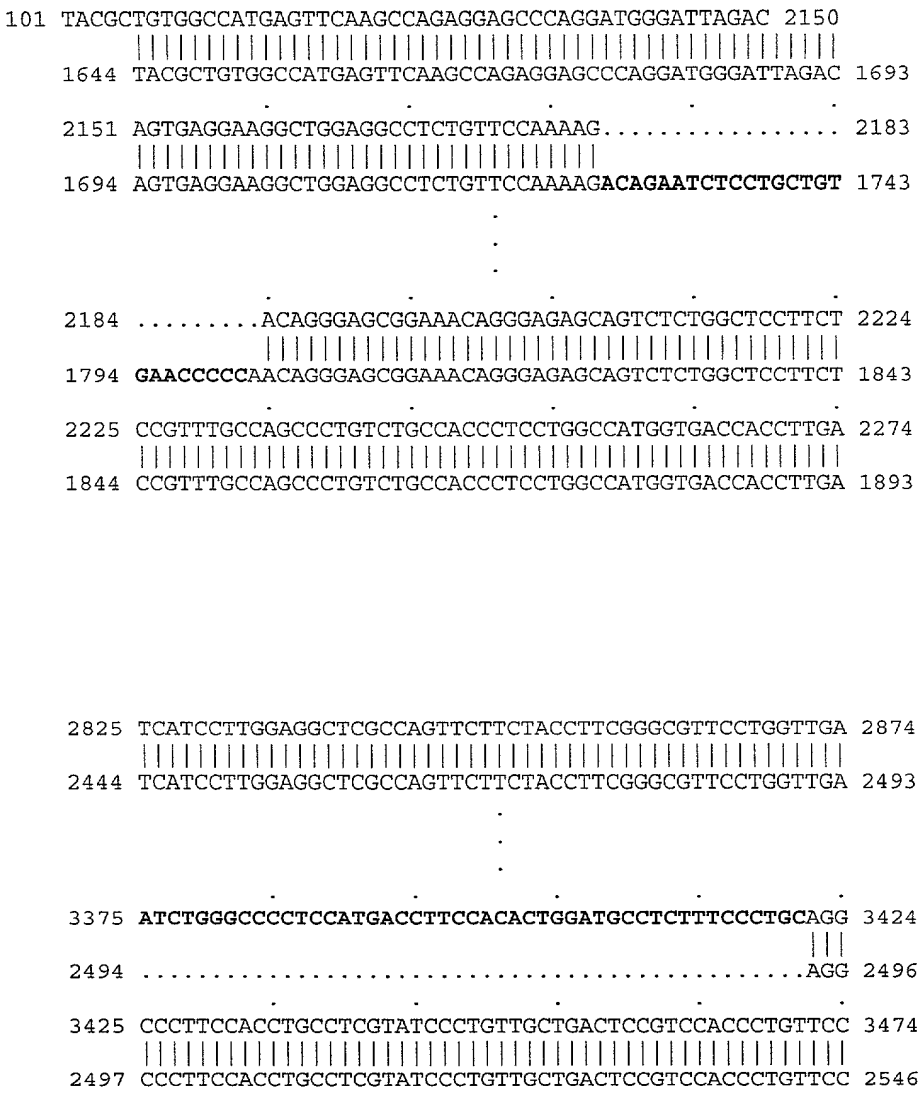
101 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 2150
1644 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 1693
2151 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAG..... 2183
1694 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGT 1743
2184 .....ACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 2224
1794 GAACCCCCAACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 1843
2225 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 2274
1844 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 1893
2825 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2874
2444 TCATCCTTGGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2493
3375 ATCTGGGCCCCTCCATGACCTTCCACACTGGATGCCTCTTTCCCTGCAGG 3424
2494 .....AGG 2496
3425 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 3474
2497 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 2546

Figure 6.

```
Query= sequence
         (1114 letters)

Database: newnr
           228,478 sequences; 162,186,938 total letters

Searching.....................................................done

                                                                    Score     E
Sequences producing significant alignments:                         (bits)  Value

gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melano...   127  5e-28
gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC3310...    68  4e-10
gb|AAF57514.1| (AE003794) CG8595 gene product [Drosophila melano...    47  0.001

>gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melanogaster]
           Length = 1289

 Score =  127 bits (317), Expect = 5e-28
 Identities = 99/321 (30%), Positives = 149/321 (45%), Gaps = 11/321 (3%)

Query: 38  KLAGLLRESGDVVXXXXXXXXXXXXXXXXXNHVF------ELHLGPWGPGQTGFVALPSH 91
           +LA LLR++GD +                  N  F      E+  G        F  +
Sbjct: 8   ELANLLRQNGDKILSSEFTLTLSGSLLRALNDSFTLIADTEIGTGAGYLQPQSFQVVKPI 67

Query: 92  PADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP-TGPIKIFPFKSLRHLELRGVPLHCLH 150
            A S V   LQ + D +QKT  LKL +         G I I  F++LR LE+  + +  +
Sbjct: 68  NAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHYFEGAIDIAKFRALRRLEVNKINIGQVV 127

Query: 151 GLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSANFSYNXXXXXXXXXXX 210
           G++ +  QL+ LIC +SL +++++++ CGGD  +   W  L +A+FSYN
Sbjct: 128 GIQPLRGQLQHLICVKSLTSVDDIITRCGGDNSNGFVWNELKTADFSYNSLRSVDTALEF 187

Query: 211 XXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGA-ALGVLILRGNE 269
                    HN++      +  L  L  LD+SYN L  +P+        L +L +  N
Sbjct: 188 AQHLQHLNLRHNKLTSVAA-IKWLPHLKTLDLSYNCLTHLPQFHMEACKRLQLLNISNNY 246

Query: 270 LRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHPEHRAATAQ 329
           +  L  + +L  L +LDL+ N L  H +L PL  L  L L L+GNPL  +P+HR ATAQ
Sbjct: 247 VEELLDVAKLDALYNLDLSDNCLLEHSQLLPLSALMSLIVLNLQGNPLACNPKHRQATAQ 306

Query: 330 YLSPRARDAATGFLLDGKVLS 350
           YL      A   F+LD + L+
Sbjct: 307 YL--HKNSATVKFVLDFEPLT 325
```

Figure 7A

```
 Score = 41.4 bits (95), Expect = 0.054
 Identities = 41/151 (27%), Positives = 62/151 (40%), Gaps = 20/151 (13%)

Query: 814  VDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLLKVTGEMRE 873
            +DHRL+L+     F +  E F+   K  +           LVV+S+ + YL++   E  +
Sbjct: 1018 IDHRLKLYFYQRKFKEDGEHFKWLAKGRIYNEQTQSLGEGLVVMSNCKCYLMEAFAEPHD 1077

Query: 874  PPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGA-------GRCVLLPRDARHCRAF 926
              A WL+  ++V +  L  I+L        L W  G         G  VLL  D
Sbjct: 1078 DVAKWLRQVVSVAVNRLVAIDL--------LPWKLGLSFTLKDWGGFVLLLHDMLR---- 1125

Query: 927  LEELLDVLQSLPPAWRNCVSATEEEVTPQHR 957
              E LL+ LQ +P     C    +  VT  H+
Sbjct: 1126 TESLLNYLQQIPLP-EQCKLNHQPSVTLSHQ 1155


>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
           (AF082516) I-1 receptor candidate protein [Homo sapiens]
           Length = 1504

 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLVHVAGP-GPTG---------PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
           +L  T  LK + V+G  GP G          P  +  FKSL  +E+        + GL
Sbjct: 180 ILDFTCRLKYLKVSGTEGPFGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICSRSLQALEELL--------------SACGGDFCSALP-WLALLSANFSYNXX 201
             L TL    S  +++E+L                +   G   + +P W AL + + S+N
Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

Query: 202 XXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
                            HN +      L  L  L HLD+SYN+L  +  +       +
Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262 VLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
            L L GN L SL GL +L +L +LDL  N +E   E+  +  L  L  + L  NPL   P
Sbjct: 359 TLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322 EHRAATAQYLSPRARD 337
           ++R          RA +
Sbjct: 419 DYRTKVLAQFGERASE 434
```

Figure 7B

```
FL1-18_SPLICE_VARIANT                ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----------
FL1-18                               ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----------
Drosophila_melanogaster_CG9044       ------MDPQK--------------ITELANLLRQNGD-----------
imidazoline_receptor_candidate       MATARTFGPEREAEPAKEARVVGSELVDTYTVYIIQVTDGSHEWTVKHRY
                                            *::         .      :   :  : :  *

FL1-18_SPLICE_VARIANT                ---------VVLSGCSTLSLLTP--------------------------
FL1-18                               ---------VVLSGCSTLSLLTP--------------------------
Drosophila_melanogaster_CG9044       ---------KILSSEFTLTLSGS--------------------------
imidazoline_receptor_candidate       SDFHDLHEKLVAERKIDKNLLPPKKIIGKNSRSLVEKREKDLEVYLQKLL
                                           : .     .*  .

FL1-18_SPLICE_VARIANT                ------TLQQLNHVFELHLG--------------------------PWG
FL1-18                               ------TLQQLNHVFELHLG--------------------------PWG
Drosophila_melanogaster_CG9044       ------LLRALNDSFTLIADT-------------------------EIG
imidazoline_receptor_candidate       AAFPGVTPRVLAHFLHFHFYEINGITAALAEELFEKGEQLLGAGEVFAIG
                                           : * . : :                                  *

FL1-18_SPLICE_VARIANT                PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
FL1-18                               PG----Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
Drosophila_melanogaster_CG9044       TGAGYLQPQSFQVVKPINAKSSVFPDLQLVHDFVQKTTLLKLTYFPSEHY
imidazoline_receptor_candidate       PLQLYAVTEQLQQGKPTCASGDAKTDLGHILDFTCRLKYLKVSGTEGPFG
                                     .         :    .  *.. .  :*  : *.  :   **:    .

FL1-18_SPLICE_VARIANT                -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
FL1-18                               -------TGPIKIFPFKSLRHLELRGVPLHCLHGLRGIYSQLETLICSRS
Drosophila_melanogaster_CG9044       F------EGAIDIAKFRALRRLEVNKINIGQVVGIQPLRGQLQHLICVKS
imidazoline_receptor_candidate       TSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASKPTLATLSVRFS
                                           .:.:  *::*:::*:       : *:      *  *    *

FL1-18_SPLICE_VARIANT                LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
FL1-18                               LQALEELLSACGGDFCSALP--------------WLALLSANFSYNALT
Drosophila_melanogaster_CG9044       LTSVDDIITRCGGDNSNGFV--------------WNELKTADFSYNSLR
imidazoline_receptor_candidate       ATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSIS
                                       ::.:::   ..:  .                  *  * : ::*:*::

FL1-18_SPLICE_VARIANT                ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
FL1-18                               ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
Drosophila_melanogaster_CG9044       SVDTALEFAQHLQHLNLRHNKLTSVA-AIKWLPHLKTLDLSYNCLTHLPQ
imidazoline_receptor_candidate       EIDESVKLIPKIEFLDLSHNGLLVVD-NLQHLYNLVHLDLSYNKLSSLEG
                                      :* ::.:   :..*:* ** :      :  * .*  **:*** *  :

FL1-18_SPLICE_VARIANT                -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
FL1-18                               -MGPSGAALGVLILRGNELRSLHGLEQLRNLRHLDLAYNLLEGHRELSPL
Drosophila_melanogaster_CG9044       FHMEACKRLQLLNISNNYVEELLDVAKLDALYNLDLSDNCLLEHSQLLPL
imidazoline_receptor_candidate       -LHTKLGNIKTLNLAGNLLESLSGLHKLYSLVNLDLRDNRIEQMEEVRSI
                                            :  * : .* :..* .: :*  * :***  * :    :: .:

FL1-18_SPLICE_VARIANT                WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
FL1-18                               WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
Drosophila_melanogaster_CG9044       SALMSLIVLNLQGNPLACNPKHRQATAQYLHKNS--ATVKFVLDFEPLTK
imidazoline_receptor_candidate       GSLPCLEHVSLLNNPLSIIPDYRTKVLAQFGERA----SEVCLDDTVTTE
                                       *  *  : * .***   *.:*  .   :  .:.:    . **    :
```

Figure 8A

```
FL1-18_SPLICE_VARIANT                TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
FL1-18                               TDFQTHTS------LGLSPMGPP-LPWPVGSTPETSGGPDLSDSLSSG--
Drosophila_melanogaster_CG9044       AEKALTGSQKWRYISGLSHRSPRSTSMSINSSSASINTSDGSQFSSFGSQ
imidazoline_receptor_candidate       KELDTVEV------LKAIQKAKE--VKSKLSNPEKKGGED-SRLSAAPCI
                                      :                .      .  *.. . .  * *   :

FL1-18_SPLICE_VARIANT                ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
FL1-18                               ------G-----VVTQPLLHKVKS-RVR---VRRASISEPS--DTD----
Drosophila_melanogaster_CG9044       RSVSIRGKNYTLEDNQSMDTSQSSKRISSCKIRTVDIEESSEINTDAASV
imidazoline_receptor_candidate       R----PSSSPPTVAPASASLPQPILSNQGIMFVQEEALASSLSSTDS---
                                           .          .                .   .   .*  .**

FL1-18_SPLICE_VARIANT                --PEPRT--------LNPSPAG-------------------WFVQQHPEL
FL1-18                               --PEPRT--------LNPSPAG-------------------WFVQQHPEL
Drosophila_melanogaster_CG9044       STPNPRSE-------YEEEPDNSHLETKKKIETLRLTYGNEWLKSGNAEL
imidazoline_receptor_candidate       LTPEHQPIAQGCSDSLESIPAG----QAASDDLRDVPGAVGGASPEHAEP
                                       *: :.          :  * .                          :.*

FL1-18_SPLICE_VARIANT                EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
FL1-18                               EL-------MSSFRERFG-------RNWLQYRSHLE---PSGNP-----L
Drosophila_melanogaster_CG9044       MLGIE--TPQPTERERNES-----RQLFNEYLGELSGFTEAKNDSEHHNI
imidazoline_receptor_candidate       EVQVVPGSGQIIFLPFTCIGYTATNQDFIQRLSTLIR--QAIERQLPAWI
                                      :                      : : :  . *     : :      :

FL1-18_SPLICE_VARIANT                PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
FL1-18                               PATPT-------TSAPSAPPASSQGPDTAPRP-----SPPQE---EARG-
Drosophila_melanogaster_CG9044       SSTPTNNVLLASTFDATITPIKSEANDTSGQTLYETCTEGEETNYESFGN
imidazoline_receptor_candidate       EAANQRE-EGQGEQGEEEDEEEEEEEDVAENRYFEMGPPDVE---EEEGG
                                      ::                   ..:  *.: .      .   *   *  *

FL1-18_SPLICE_VARIANT                ------PQESPQ-KMSEEVRAEP----QEEEE----------------E
FL1-18                               ------PQESPQ-KMSEEVRAEP----QEEEE----------------E
Drosophila_melanogaster_CG9044       NTTELSTEERPPDRHEELLRLYASSSNAQDED----------------P
imidazoline_receptor_candidate       GQGE-EEEEEEEDEEAEEERLALEWALGADEDFLLEHIRILKVLWCFLIH
                                            :*    .  *  *         :*:

FL1-18_SPLICE_VARIANT                KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
FL1-18                               KEGKEEKEEGEMV--EQGEEEAGEEEEEEQ-DQKEVEAEL----CRP---
Drosophila_melanogaster_CG9044       VSDAESDEETYIVYHEQKPSEVLFLTISSN-FIREKDTLT----ERT---
imidazoline_receptor_candidate       VQGSIRQFAACLVLTDFGIAVFEIPHQESRGSSQHILSSLRFVFCFPHGD
                                      ..   .    :*  :            ...   :.  :         .

FL1-18_SPLICE_VARIANT                LLVCPLEGPEG-----VRGRECFLRVTSA----HLFEVEL------QAAR
FL1-18                               LLVCPLEGPEG-----IRGRECFLRVTSA----HLFEVEL------QAAR
Drosophila_melanogaster_CG9044       KAKWSLKILESC----ERVRSNTLRINFD----TMRKDKQ------ERIY
imidazoline_receptor_candidate       LTEFGFLMPELCLVLKVRHSENTLFIISDAANLHEFHADLRSCFAPQHMA
                                          :   *       *  .  * :           . .       :

FL1-18_SPLICE_VARIANT                TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
FL1-18                               TLERLELQSLEAAEIEPEAQAQRSPRPTGS------DLLPGAPIL-----
Drosophila_melanogaster_CG9044       CVENTLCQELEKKLRDILSQRDLTEMNISIYRCV--NCLTQFTIEQK---
imidazoline_receptor_candidate       MLCSPILYGSHTSLQEFLRQLLTFYKVAGGCQERSQGCFPVYLVYSDKRM
                                      :        .    :   *        .        . :.   :
```

Figure 8B

```
FL1-18_SPLICE_VARIANT              ----SLRFS-----YICPDRQ-------------LRR----YLVLEP-DA
FL1-18                             ----SLRFS-----YICPDRQ-------------LRR----YLVLEP-DA
Drosophila_melanogaster_CG9044     ----SKRYKA--KELRCPDCRSVYVAEVTELSSSLSKPS-GEVAAEPKLS
imidazoline_receptor_candidate     VQTAAGDYSGNIEWASCTLCSAVRRSCCAPSEAVKSAAIPYWLLLTPQHL
                                       :  :.       *.                          :   *

FL1-18_SPLICE_VARIANT              HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
FL1-18                             HAAVQELLAVLTPVTNVAREQ-------LGEARDLLLGRFQC-------L
Drosophila_melanogaster_CG9044     PAMIVEESPVEELAAAINKEES----NSIGKSLASFLFYFDESSFDSNQS
imidazoline_receptor_candidate     NVIKADFNPMPNRGTHNCRNRNSFKLSRVPLSTVLLDPTRSCTQ-PRGAF
                                     .   :  .:    :   ::.       :  :   :    .

FL1-18_SPLICE_VARIANT              RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTESPAVCP
FL1-18                             RCG--------HEFKPEEPRMGLDSE------EGWRP-LFQKTGS-----
Drosophila_melanogaster_CG9044     VVGSSNTDRD-MEFRANESDVDIISNPSQSSIEVLDPNYVQSASRKTSEE
imidazoline_receptor_candidate     ADGHVLELLVGYRFVTAIFVLPHEKFHFLRVYNQLRA-SLQDLKTVVIAK
                                     *         .* .    :   .       :   .  .*.

FL1-18_SPLICE_VARIANT              NCGSDHVVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRA
FL1-18                             --GNRESSLWLLLR-LP---------ALSATLLAMVTTLTGPRTAHL-RH
Drosophila_melanogaster_CG9044     RRISQLPHLETIHDEVAK-SKSFIEREFGQLLAEQAQPTTPSTAAPLAPA
imidazoline_receptor_candidate     TPGTGGSPQGSFADGQPAERRASNDQRPQEVPAEALAPAPVEVPAPAPAA
                                      .       .    . . .   :.          .

FL1-18_SPLICE_VARIANT              KNSP-P-QAPSTRDHGSW------------SLSPPPERCGLRSVDHRLRL
FL1-18                             R-------APVTMVVG--------------ASVPP--------------
Drosophila_melanogaster_CG9044     KSAV-PSHVPLTESSSSGSVTDSICTTYEQQATDAPQNLQNSLLTESSNS
imidazoline_receptor_candidate     ASASGPAKTPAPAEASTSALVP--EETPVEAPAPPPAEAPAQYPSEHLIQ
                                     .      ..* .   .                  : .* .       .

FL1-18_SPLICE_VARIANT              FLDVEV-----FSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLL
FL1-18                             -------------------------LSAVAS-------ALWTTDS-----
Drosophila_melanogaster_CG9044     QVSGSD-----AESNSRLKSAEDASLLPFASVFQSTNLLMSSSKKLIESE
imidazoline_receptor_candidate     ATSEENQIPSHLPACPSLRHVASLRGSAIIELFHSSIAEVENEELRHLMW
                                     . .                          ..      .    :   .

FL1-18_SPLICE_VARIANT              KVTGEMREPPASWLQLTLAVPLQDLSGIELGL---AGQSLRLEWAAGAG-
FL1-18                             ---------GSSWMLRCSAMPRRSSS---------AASRCQWHWQATLGS
Drosophila_melanogaster_CG9044     ATVFGTQPYKFNYSDFNDIDHRLKLYFYQRKF---KEDGEHFKWLAKGRI
imidazoline_receptor_candidate     SSVVFYQTPGLEVTACVLLSTKAVYFVLHDGLRRYFSEPLQDFWHQKNTD
                                         .    .                .         .  :  *

FL1-18_SPLICE_VARIANT              -------RCVLLPRDARHCRAFLEELLDVLQSLPPAWRNCVS--ATEEEV
FL1-18                             -------SCALWLCLTAGCTC----------------------------
Drosophila_melanogaster_CG9044     YN-EQTQSLGEGLVVMSNCKCYLMEAFAEPHDDVAKWLRQVVSVAVNRLV
imidazoline_receptor_candidate     YNNSPFHISQCFVLKLSDLQSVNVGLFDQHFRLTGSTPMQVVTCLTRDSY
                                                          .                    .

FL1-18_SPLICE_VARIANT              TPQHRLWPLLEKDSSLEARQFFYLR----------AFLVEGPSTCLVS--
FL1-18                             ------------------------------------------------
Drosophila_melanogaster_CG9044     AIDLLPWKLGLSFTLKDWGGFVLLLHDMLRTESLLNYLQQIPLPEQCK--
imidazoline_receptor_candidate     LTHCFLQHLMVVLSSLERTPSPEPVDKDFYSEFGNKTTGKMENYELIHSS
                                     .              :                    :
```

Figure 8C

```
FL1-18_SPLICE_VARIANT                --LLLTPS------TLFLLDEDAAGSP----------------AEPS---
FL1-18                               --------------------------------------------------
Drosophila_melanogaster_CG9044       --LNHQPS------VTLSHQWETIASEPVKMCSLIPSCQWICDQEKSS--
imidazoline_receptor_candidate       RVKFTYPSEEEIGDLTFTVAQKMAEPEKAPALSILLYVQAFQVGMPPPGC
                                            .             .

FL1-18_SPLICE_VARIANT                -----PPAASGEASEKVPPSGPG----PAVRVREQ---QPLSSLSS----
FL1-18                               --------------------------------------------------
Drosophila_melanogaster_CG9044       ----FEPSLLLITETHLYISGNGKFSWLSDKVQEKP-IQPELSLNQP---
imidazoline_receptor_candidate       CRGPLRPKTLLLTSSEIFLLDEDCVHYPLPEFAKEPPQRDRYRLDDGRRV
                                                  . .              .  ::   .     ..

FL1-18_SPLICE_VARIANT                ------VLLYRSAPEDLRLLFYD----------------EV--------S
FL1-18                               --------------------------------------------------
Drosophila_melanogaster_CG9044       --LSNLVDVERITDQKYAINFID----------------ET--------Q
imidazoline_receptor_candidate       RDLDRVLMGYQTYPQALTLVFDDVQGHDLMGSVTLDHFGEVPGGPARASQ
                                               .   :       :                :         .

FL1-18_SPLICE_VARIANT                RLESFWALRVVCQEQLTALLAWIREPWEELFSIGLRTVIQEALALDR
FL1-18                               -----------------------------------------------
Drosophila_melanogaster_CG9044       NRCEIWKLQFETHANAACCLNVIGKGWEQLFGVPFSLSGT-------
imidazoline_receptor_candidate       GREVQWQVFVPSAESREKLISLLARQWEALCGRELPVELTG------
                                      .         .  :                 :.
```

(* REPRESENTS RESIDUES THAT ARE IDENTICAL IN ALL FOUR PRTEINS; : REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CHARACTER IN 3 OUT OF THE 4 PROTEINS; . REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CAHARACTER IN 2 OUT OF THE 4 PROTEINS).

Figure 8D

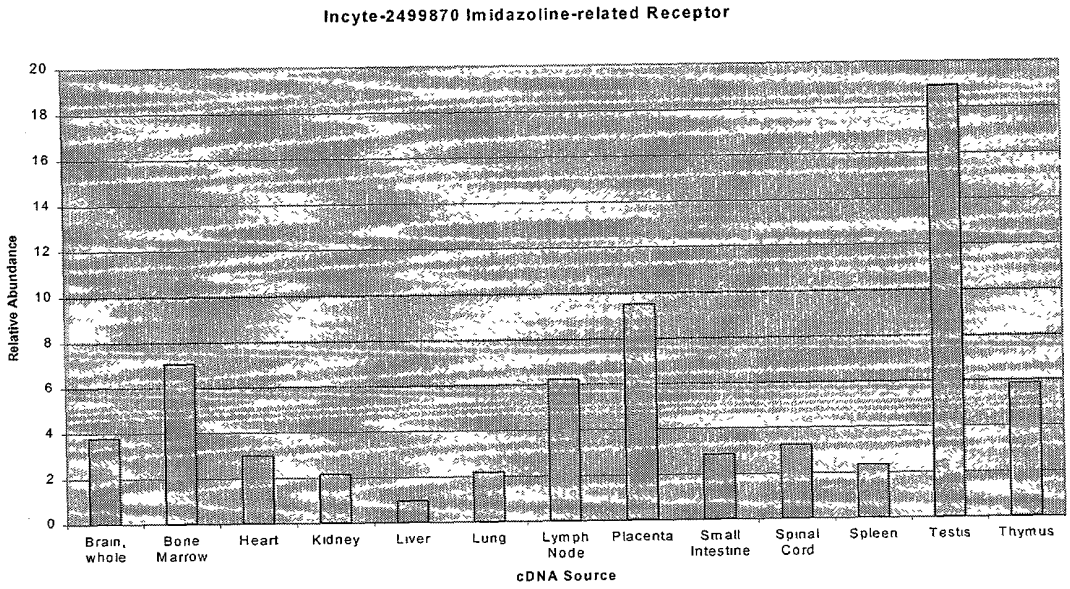
Incyte-2499870 Imidazoline-related Receptor
Relative Abundance
20
18
16
14
12
10
8
6
4
2
0
Brain, whole
Bone Marrow
Heart
Kidney
Liver
Lung
Lymph Node
Placenta
Small Intestine
Spinal Cord
Spleen
Testis
Thymus
cDNA Source

Figure 9.

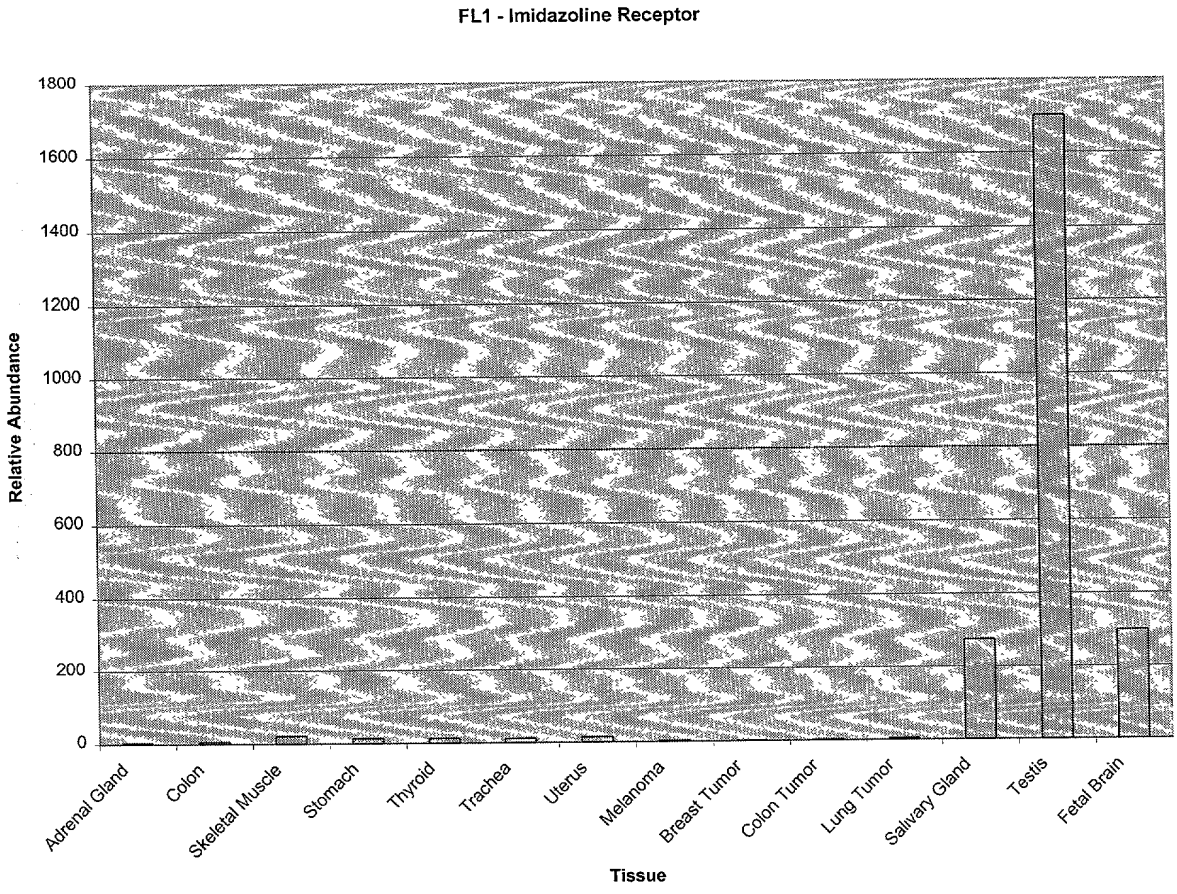
FL1 - Imidazoline Receptor
Relative Abundance
1800
1600
1400
1200
1000
800
600
400
200
0
Adrenal Gland
Colon
Skeletal Muscle
Stomach
Thyroid
Trachea
Uterus
Melanoma
Breast Tumor
Colon Tumor
Lung Tumor
Salivary Gland
Testis
Fetal Brain
Tissue

Figure 10.